

GenCore version 5.1.7
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ALIGNMENT!

Sequence	13,	Appl
Sequence	11,	Appl
Sequence	7,	Appl
Sequence	8,	Appl
Sequence	7,	Appl
Sequence	8,	Appl
Sequence	2,	Appl
Sequence	2,	Appl
Sequence	3,	Appl
Sequence	8,	Appl
Sequence	7,	Appl
Sequence	9,	Appl
Sequence	4,	Appl
Sequence	4,	Appl
Sequence	1544,	Appl
Sequence	5,	Appl
Sequence	5,	Appl

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Gencore version 5.1.7

Total number of hits satisfying chosen parameters: 572060

Title: US-10-666-851-2
Perfect score: 1706
Sequence: 1 MGIGRSEGCGRRGAGVLLA. KNPFMKKOMKHNICPPTFQSVDK 314
Scoring table: BLOSUM62
Gapop 10.0 , **Gapext** 0.5

XX
 PT New secreted Frizzled-related protein-1-binding Peptide, for enhancing or
 PT stimulating osteoclast differentiation or to modify T-cell activity in a
 PT subject with e.g. abnormal bone remodeling, achondroplasia or
 PT osteopetrosis.
 XX
 PG Example; Page 74-75; 81pp; English.
 XX
 CC The invention relates to a purified Peptide that binds to secreted
 CC Frizzled-related protein (sFRP)-1. The peptide is useful for enhancing or
 CC stimulating osteoclast differentiation, or to modify T-cell activity in a
 CC subject with abnormal bone remodeling, achondroplasia, Albright's
 CC osteodystrophy or osteopetrosis. The sFRP-1 is useful for inhibiting
 CC osteoclast formation in a subject with a bone disorder or unwanted bone
 CC resorption, e.g. postmenopausal osteoporosis, Paget's disease, lytic bone
 CC metastases, multiple myeloma, rheumatoid arthritis, hypercalcemia of
 CC malignancy. Modulating T-cell activity is useful in subjects suspected of
 CC having toxic shock, sepsis, graft-versus-host reactions or acute
 CC inflammatory reactions. The immunostimulatory sFRP-1-binding peptide is
 CC useful in activating the immune system against bacterial, viral and
 CC parasitic infections, and in the treatment of human immunodeficiency
 CC virus (HIV). The present sequence represents a human sFRP-1 netrin
 CC homology domain
 XX
 SQ Sequence 141 AA;
 XX
 ID AAY48493 100.0%; Score 78; DB 5; Length 141;
 AC AAY48493; Best Local Similarity 100.0%; Pred. No. 0.00046;
 XX DT 08-DBC-1999 (first entry)
 KW Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 OY 1 KKENGDDKKVPKKKK 15
 DB 52 KKENGDDKKVPKKKK 66
 XX
 RESULT 2
 AAY48493
 ID AAY48493 standard; protein; 148 AA.
 AC AAY48493;
 XX
 DT 08-DBC-1999 (first entry)
 KW Human breast tumour-associated protein 38.
 KW Expressed sequence tag; EST; human; breast; cancer; cytostatic;
 KW medicaments; gene therapy; treatment; fat metabolism.
 XX Homo sapiens.
 OS DE319813835-A1.
 XX PN DE319813835-A1.
 XX PD 23-SEP-1999.
 XX PR 20-MAR-1998; 98DB-01013835.
 XX PR 20-MAR-1998; 98DB-01013835.
 XX PA (MESTA-) METAGEN GES GENOMFORSCHUNG MBH.
 XX PI Specht T, Hinzmam B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 XX DR MPI, 1999-528979/45.
 XX DR N-PGDB, ARZ33577.
 XX Human nucleic acid sequences and protein products from normal breast
 PT tissue, useful for breast cancer therapy.
 XX Claim 28, 175, 206pp; German.
 PS
 XX
 CC This invention describes novel human nucleic acid sequences from normal
 CC breast tissue which have cytostatic activity. The nucleic acid sequences
 CC can be used to produce and isolate full-length gene sequences. They can

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OM protein - protein search, using SW model
Run on: May 5, 2006, 13:50:51 ; Search time 229 seconds
(without alignment)
96.7406 Million cell updates/sec

Title: US-10-666-851-2

perfect score: 1706

Sequence: 1 MGIGRSRRGAAAGVLLA.....KNFNMKMKHBCPTQSVFK 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05_80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1706	100.0	314	1 SFRP1_HUMAN	Q8a474 homo sapien
2	1626	95.3	314	2 Q50542_MOUSE	Q50542 mus musculus
3	1623	95.1	314	1 SFRP1_MOUSE	Q8e4u3 mus musculus
4	1607	94.2	308	1 SFRP1_BOVIN	Q91166 bos taurus
5	1489	87.3	314	1 SFRP1_CHICK	Q9deq4 gallus gallus
6	1100	64.5	305	2 Q6GZL1_ORVALIA	Q6gzk1 oryzias latipes
7	1092	64.0	321	2 Q9SK03_TETRAODON	Q48ic3 tetradon nigrum
8	1084	63.9	311	2 Q9Y124_XENLA	Q9y124 xenopus laevis
9	1070	62.7	310	2 Q6YMR8_BRARE	Q6ymr8 brachydanio
10	1012	59.3	296	2 Q7T2K9_BRARE	Q7t2k9 brachydanio
11	955	56.0	311	2 Q4R9B2_TETING	Q4rgb2 tetradon nigrum
12	947	55.5	281	2 Q5FBX0_BRARE	Q5fbx0 brachydanio
13	946	55.5	315	2 Q6GL50_XENLA	Q6gj50 xenopus laevis
14	945	55.4	315	2 Q6A0J3_XENLA	Q6a0j3 xenopus laevis
15	942	55.2	315	2 Q8AMC4_XENLA	Q8amc4 xenopus laevis
16	924	54.2	317	1 SFRP5_HUMAN	Q5fa47 homo sapien
17	922	54.1	314	1 SFRP5_MOUSE	Q9mu66 mus musculus
18	916	53.7	315	1 SFRP5_BOVIN	Q9rc11 bos taurus
19	844	49.5	158	1 SFRP1 RAT	Q9rl68 rattus norvegicus
20	718	42.1	178	2 Q6SL14_HUMAN	Q6sal4 homo sapiens
21	658	38.6	295	2 Q6PB88_XENTR	Q6pb88 xenopus tropicalis
22	649	38.0	295	2 Q4SS00_TETING	Q4ss00 tetradon nigrum
23	645	37.8	298	2 Q7ZXN6_XENLA	Q7zxn6 xenopus laevis
24	629	36.9	282	2 Q8JHC7_BRARE	Q8jhc7 brachydanio
25	610	35.8	294	1 SFRP2_CANFA	Q8g3h1 canis familiaris
26	610	35.8	365	2 Q4H2U5_CLODN	Q4h2u5 cicuta intesta
27	605	35.5	292	1 SFRP2_CHICK	Q4tcbn1 gallus gallus
28	605	35.5	295	1 SFRP2_MOUSE	Q97299 mus musculus
29	602	35.3	295	1 SFRP2_HUMAN	Q96ft1 homo sapiens
30	595	34.9	283	2 Q9BG66_RABIT	Q9q986 oryctolagus cuniculus
31	541	31.7	307	2 Q42397_CHICK	Q42397 gallus gallus

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Maximum Match 100%
Listing first 45 summaries

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21	658	38.6	295	2 Q6PB88_XENTR	Q6pb88 xenopus tropicalis
22	649	38.0	295	2 Q4SS00_TETING	Q4ss00 tetradon nigrum
23	645	37.8	298	2 Q7ZXN6_XENLA	Q7zxn6 xenopus laevis
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Maximum Match 100%
Listing first 45 summaries

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05_80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1489	87.3	314	1 SFRP1_CHICK	Q9deq4 gallus gallus
6	1100	64.5	305	2 Q6GZL1_ORVALIA	Q6gzk1 oryzias latipes
7	1092	64.0	321	2 Q9SK03_TETRAODON	Q48ic3 tetradon nigrum
8	1084	63.9	311	2 Q9Y124_XENLA	Q9y124 xenopus laevis
9	1070	62.7	310	2 Q6YMR8_BRARE	Q6ymr8 brachydanio
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23	645	37.8	298	2 Q7ZXN6_XENLA	Q7zxn6 xenopus laevis
24	629	36.9	282	2 Q8JHC7_BRARE	Q8jhc7 brachydanio
25	610	35.8	294	1 SFRP2_CANFA	Q8g3h1 canis familiaris
26	610	35.8	365	2 Q4H2U5_CLODN	Q4h2u4 cicuta intesta
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31	541	31.7	307	2 Q42397_CHICK	Q42397 gallus gallus

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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GenCore version 5.1.7

OM protein - protein search, using SW model
Run on: May 5, 2006, 13:54:06 ; Search time 39 seconds
(without alignments)

Title: US-10-666-851-2
perfect score: 1706
Sequence: 1 MGIGRSEGRGALGVLIA..... KNFMKMMKHNHCPTQSVFK 314

Scoring table: BL2US62
GapOp 10.0 , Gapext 0.5

Searched: 283416 seqs., 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.0:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB	ID	Description
1	917.5	MGIGRSEGRGALGVLIA..... KNFMKMMKHNHCPTQSVFK	317	PIR	JE0175	frizzled protein-1b - human
2	35.0	317	2	PIR	JE0175	frizzled protein-1
3	35.0	295	2	PIR	JE0174	frizzled protein-2
3	276.5	16.2	574	2	JE0339	Frizzled-7 protein
4	273.5	16.0	568	2	T25162	Frizzled-1 protein
5	271.5	15.9	537	2	JC7127	frizzled protein 4
6	265	15.5	647	2	JB0337	Frizzled-1 protein
7	264	15.5	581	2	S03540	gene frizzled prot
8	258	15.1	565	2	JE0338	Frizzled-2 protein
9	256.5	15.0	581	2	JC7086	PDZ10 protein - hu
10	222.5	14.8	641	2	A45054	probable intercell
11	237.5	13.9	550	2	T37325	wingless protein
12	228.5	13.4	694	2	S71786	wingless receptor
13	223.5	13.1	197	2	JC7735	frizzled-related p
14	215	12.6	666	2	JC7712	frizzled-3 protein
15	215	12.6	705	2	JR0164	frizzled-6 protein
16	201	11.8	605	2	T31990	hypothetical prote
17	201	11.3	705	2	JB0315	low-density lipop
18	170.5	10.0	1774	2	B56101	collagen alpha 1(X)
19	133.5	7.8	526	2	T13484	frizzled protein h
20	132.5	7.8	579	2	JC7629	membrane-type friz
21	125	7.3	793	2	JC5539	Smoothened protein
22	107.5	6.3	549	2	E86337	hypothetical prote
23	97	5.7	785	2	S46672	hypothetical prote
24	97	5.7	2228	2	T14029	variant-specific s
25	96.5	5.7	1024	2	S71804	receptor-like serp
26	96.5	5.7	1150	2	T15277	hypothetical prote
27	93.5	5.5	1474	2	D88550	protein ZC84 6 [im
28	93	5.5	527	1	SARUP	saposin precursor
29	92.5	5.4	1051	2	JC4091	glycoprotein A - p

ALIGNMENTS

30	91	5.3	260	2	T01837	hypothetical prote
31	91	5.3	527	2	A42032	epidermal growth f
32	91	5.3	1008	2	CB4679	hypothetical prote
33	91	5.3	1077	2	T21800	hypothetical prote
34	91	5.3	1223	1	TVERLV	epidermal growth f
35	90.5	5.3	1751	2	T09394	gag-pro-pol polyP
36	89.5	5.2	792	2	A70476	ATP-dependent DNA
37	88	5.2	718	2	T51488	hypothetical prote
38	88	5.2	1051	2	S55259	TIP1 protein - mou
39	87.5	5.1	1097	2	A56138	transcription fact
40	87.5	5.1	4152	2	T31102	filamentous hemagg
41	87.5	5.1	4919	2	T31105	hypothetical prote
42	87	5.1	578	2	C64525	restriction modifi
43	87	5.1	1699	2	T14074	complement compone
44	86.5	5.1	623	2	A49112	sodium-glucose cot
45	86.5	5.1	1001	2	S30385	G9a protein - huma

RESULT 2
Species: Homo Sapiens (man)
CDate: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004

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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:50:11 ; Search time 186 Seconds
 (without alignments)
 741.747 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706

Sequence: MGIGRSECRRGALGAALVILIA.....KNPFMKSGMMNNHBCPTFQSVFK 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqB, 4393781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 0

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

A_Geneseq_21: *
 1: geneseqD1980a: *
 2: geneseqD1990a: *
 3: geneseqD2000a: *
 4: geneseqD2001a: *
 5: geneseqD2002a: *
 6: geneseqD2003a: *
 7: geneseqD2003ba: *
 8: geneseqD2004a: *
 9: geneseqD2005a: *

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SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULTS

Key	Location/Qualifiers
FT Peptide	1..28 /note= "putative signal sequence"
FT Misc-difference	14 /note= "encoded by a cAG insertion sequence observed in some cDNA constructs"
FT Protein	29..314 /note= "mature protein"
FT Domain	57..166 /note= "Wnt binding domain"
FT Modified-site	173..175 /note= "Abn is potentially N-glycosylated"
FT Modified-site	263..265 /note= "Abn is potentially N-glycosylated"
FT PTN	W09854325-A1.
FT PDD	03-DRC-1998.
FT PFP	29-MAY-1998; 98WMO-US010974.
FT PR	29-MAY-1997; 97US-0050417P.
FT PR	23-JUN-1997; 97US-0050495P.
FT XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
FT PR	Rubin JS, Finch P, Aaronson S, He X;
DR	WPI; 1999-05940/05.
DR	N-PSDB; AAV84395.

RESULTS

Key	Location/Qualifiers
FT Peptide	1..28 /note= "putative signal sequence"
FT Misc-difference	14 /note= "encoded by a cAG insertion sequence observed in some cDNA constructs"
FT Protein	29..314 /note= "mature protein"
FT Domain	57..166 /note= "Wnt binding domain"
FT Modified-site	173..175 /note= "Abn is potentially N-glycosylated"
FT Modified-site	263..265 /note= "Abn is potentially N-glycosylated"
FT PTN	W09854325-A1.
FT PDD	03-DRC-1998.
FT PFP	29-MAY-1998; 98WMO-US010974.
FT PR	29-MAY-1997; 97US-0050417P.
FT PR	23-JUN-1997; 97US-0050495P.
FT XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
FT PR	Rubin JS, Finch P, Aaronson S, He X;
DR	WPI; 1999-05940/05.
DR	N-PSDB; AAV84395.

Result No.	Score	Query	Match Length	DB ID	Description
1	1706	100.0	314	2 AAW88528	Raw88528 Human Pri
2	1706	100.0	314	6 ABP77273	Abp77273 Human BFR
3	1706	100.0	314	8 ADP6536	Adp6536 Human sec
4	1706	100.0	314	8 ADP99142	Adr99142 Secreted
5	1701	99.7	314	2 AAW3817	Aaw3817 Human sec
6	1701	99.7	314	6 ABP72785	Abp72785 Human sec
7	1691.5	99.2	313	4 ABP10154	Aab0154 Human sec
8	1691.5	99.2	313	4 AAU07695	Aau07695 Human Pri
9	1691.5	99.2	313	6 ABP72784	Abp72784 Human sec
10	1691.5	99.2	313	7 ABR61248	Abr61248 Human emb
11	1691.5	99.2	313	8 ADP68341	Adp68341 Human sec
12	1691.5	99.2	313	8 ADU6503	Adu6503 Human sec
13	1691.5	99.2	313	8 AEA64566	Aea64566 Human lyp
14	1691.5	99.2	313	9 ADV44810	Adv44810 Secreted
15	1691.5	99.2	313	9 ADR89116	Adx89116 Human reg
16	1691.5	99.2	313	5 ABB82244	Abb82244 Human sec
17	1691.5	99.2	313	7 ADC71186	Adc71186 Human sec
18	1691.5	99.2	313	8 ADH43308	Adh43308 Human sec
19	1691.5	97.2	338	5 ABB82245	Abb82245 Human sec
20	1657.5	97.2	338	7 ADC71187	Adc71187 Human BFR
21	1657.5	97.2	338	8 ADH43309	Adh43309 Human BFR
22	1654	95.8	362	8 ABB82799	Abb82799 Human dia
23	1624	95.2	314	7 ABR61429	Abr61429 Murine em
24	1623	95.1	314	7 ABR61427	Abr61427 Murine em

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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:59:36 ; Search time 27 Seconds

Perfect score: US-10-666-851-2

Sequence: 1 MGIGRSECCRAGLVLA.....KVNPKVKHCEPFIQSVFK 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 235405 seqs, 42284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query Match Length	DB ID	Description
1	1651.5	99.2	413	9 US-10-821-234-989
2	605.5	35.9	295	11 US-11-067-21-2
3	602	35.3	295	11 US-11-067-121-11
4	602	35.3	295	11 US-11-067-121-11
5	598	35.1	295	11 US-10-216-161A-415
6	389.5	22.8	180	11 US-11-051-720-1306
7	298	17.5	117	11 US-11-054-281-306
8	290	17.0	586	11 US-11-054-281-93
9	280	16.4	530	11 US-11-054-281-94
10	271.5	15.9	537	8 US-10-511-937-2607
11	271.5	15.9	537	11 US-11-152-366-43
12	271.5	15.9	537	11 US-11-169-041-132
13	271.5	15.9	537	11 US-11-169-041-134
14	268.5	15.7	580	11 US-11-054-281-95
15	267.5	15.7	592	11 US-11-054-281-97
16	266.5	15.6	585	11 US-11-054-281-92
17	262	15.4	591	11 US-11-054-281-36
18	262	15.4	591	11 US-11-054-281-128
19	261.5	15.3	188	11 US-11-152-366-249
20	259.5	15.2	592	11 US-11-054-281-126
21	258	15.1	319	11 US-11-184-005-7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1651.5	99.2	413	9 US-10-821-234-989
2	605.5	35.9	295	11 US-11-067-21-2
3	602	35.3	295	11 US-11-067-121-11
4	602	35.3	295	11 US-11-067-121-11
5	598	35.1	295	11 US-10-216-161A-415
6	389.5	22.8	180	11 US-11-051-720-1306
7	298	17.5	117	11 US-11-054-281-306
8	290	17.0	586	11 US-11-054-281-93
9	280	16.4	530	11 US-11-054-281-94
10	271.5	15.9	537	8 US-10-511-937-2607
11	271.5	15.9	537	11 US-11-152-366-43
12	271.5	15.9	537	11 US-11-169-041-132
13	271.5	15.9	537	11 US-11-169-041-134
14	268.5	15.7	580	11 US-11-054-281-95
15	267.5	15.7	592	11 US-11-054-281-97
16	266.5	15.6	585	11 US-11-054-281-92
17	262	15.4	591	11 US-11-054-281-36
18	262	15.4	591	11 US-11-054-281-128
19	261.5	15.3	188	11 US-11-152-366-249
20	259.5	15.2	592	11 US-11-054-281-126
21	258	15.1	319	11 US-11-184-005-7

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	1651.5	99.2	413	9 US-10-821-234-989
2	605.5	35.9	295	11 US-11-067-21-2
3	602	35.3	295	11 US-11-067-121-11
4	602	35.3	295	11 US-11-067-121-11
5	598	35.1	295	11 US-10-216-161A-415
6	389.5	22.8	180	11 US-11-051-720-1306
7	298	17.5	117	11 US-11-054-281-306
8	290	17.0	586	11 US-11-054-281-93
9	280	16.4	530	11 US-11-054-281-94
10	271.5	15.9	537	8 US-10-511-937-2607
11	271.5	15.9	537	11 US-11-152-366-43
12	271.5	15.9	537	11 US-11-169-041-132
13	271.5	15.9	537	11 US-11-169-041-134
14	268.5	15.7	580	11 US-11-054-281-95
15	267.5	15.7	592	11 US-11-054-281-97
16	266.5	15.6	585	11 US-11-054-281-92
17	262	15.4	591	11 US-11-054-281-36
18	262	15.4	591	11 US-11-054-281-128
19	261.5	15.3	188	11 US-11-152-366-249
20	259.5	15.2	592	11 US-11-054-281-126
21	258	15.1	319	11 US-11-184-005-7

SEQUENCES

Result No.	Score	Query Match Length	DB ID	Description
1	1651.5	99.2	413	9 US-10-821-234-989
2	605.5	35.9	295	11 US-11-067-21-2
3	602	35.3	295	11 US-11-067-121-11
4	602	35.3	295	11 US-11-067-121-11
5	598	35.1	295	11 US-10-216-161A-415
6	389.5	22.8	180	11 US-11-051-720-1306
7	298	17.5	117	11 US-11-054-281-306
8	290	17.0	586	11 US-11-054-281-93
9	280	16.4	530	11 US-11-054-281-94
10	271.5	15.9	537	8 US-10-511-937-2607
11	271.5	15.9	537	11 US-11-152-366-43
12	271.5	15.9	537	11 US-11-169-041-132
13	271.5	15.9	537	11 US-11-169-041-134
14	268.5	15.7	580	11 US-11-054-281-95
15	267.5	15.7	592	11 US-11-054-281-97
16	266.5	15.6	585	11 US-11-054-281-92
17	262	15.4	591	11 US-11-054-281-36
18	262	15.4	591	11 US-11-054-281-128
19	261.5	15.3	188	11 US-11-152-366-249
20	259.5	15.2	592	11 US-11-054-281-126
21	258	15.1	319	11 US-11-184-005-7

OM protein - protein search, using sw model	
Run on:	May 5, 2006, 13:58:41 ; Search time 164 Seconds (without alignments) 799.990 Million cell updates/sec
Title:	US-10-666-851-2
Perfect score:	1705
Sequence:	MGIGRSBGGRRGAGVNLIA.....KNPWKKMKNHECPFQSVFK 314
Scoring table:	BLOSUM62
Gapp:	Gapp 10.0 , Gapext 0.5
Searched:	1867569 seqb, 41782326 residues
Total number of hits satisfying chosen parameters:	1867569
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database :	Published Applications AA_Main,*
1:	/cgn2_6/ptodata/1/pubpaas/US08_PUBCOMB.pep:*
2:	/cgn2_6/ptodata/1/pubpaas/US08_PUBCOMB.pep:*
3:	/cgn2_6/ptodata/1/pubpaas/US10A_PUBCOMB.pep:*
4:	/cgn2_6/ptodata/1/pubpaas/US10B_PUBCOMB.pep:*
5:	/cgn2_6/ptodata/1/pubpaas/US11_PUBCOMB.pep:*
6:	/cgn2_6/ptodata/1/pubpaas/US11_PUBCOMB.pep:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Score
1	1706
2	1706
3	1706
4	1701
5	1701
6	1701
7	1691.5
8	1691.5
9	1691.5
10	1691.5
11	1691.5
12	1691.5
13	1657.5
14	1657.5
15	1657.5
16	1657.5
17	1623
18	1267.5
19	1267.5
20	1171
21	1171
22	971
23	971
24	924.5
25	924.5
26	924.5
27	924.5
Result No.	Score
Match Length	DB ID
314	4 US-10-138-434A-3
314	4 US-10-666-851-2
314	4 US-10-788-792-148
314	4 US-10-146-474-7
314	4 US-10-146-474-7
314	5 US-10-756-149-5611
313	3 US-03-796-008-2
313	4 US-10-138-434A-4
313	4 US-10-666-851-7
313	4 US-10-786-720-3
313	4 US-10-817-525-2
313	5 US-10-847-972-77
313	4 US-10-425-586-3
313	4 US-10-466-136-3
338	4 US-10-425-586-4
338	4 US-10-466-136-4
314	5 US-10-847-972-80
267	4 US-10-425-586-7
267	4 US-10-466-136-7
246	4 US-10-425-586-6
246	4 US-10-466-136-6
246	4 US-10-466-136-6
229	4 US-10-425-586-8
229	4 US-10-466-136-8
317	4 US-10-146-474-6
317	4 US-10-338-604-2
317	4 US-10-301-764-6
317	4 US-10-768-566-1
5	US-10-768-566-1
DESCRIPTION	
SEQ ID NO 3	Publication No. US20030175864A1
GENERAL INFORMATION:	
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF HEALTH AND HUMAN SERVICES	
APPLICANT: Rubin, Jeffrey S.	
APPLICANT: Finch, Paul	
APPLICANT: Aaronson, Stuart	
APPLICANT: He, Xilin	
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN FRP AND FRAGMENTS THEREOF	
CURRENT APPLICATION NUMBER: US10/138,434A	
CURRENT FILING DATE: 2002-05-03	
PRIOR APPLICATION NUMBER: US 09/087,031	
PRIOR FILING DATE: 1998-05-29	
PRIOR APPLICATION NUMBER: US 60/050,495	
PRIOR FILING DATE: 1997-06-23	
PRIOR APPLICATION NUMBER: US 60/050,417	
PRIOR FILING DATE: 1997-05-29	
NUMBER OF SEQ ID NOS: 27	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 3	
LENGTH: 314	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1706; DB 4; Length 314;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 314; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1691; DB 4; Length 313;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 313; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 312;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 312; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 311;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 311; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 310;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 310; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 309;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 309; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 308;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 308; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 307;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 307; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 306;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 306; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 305;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 305; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 304;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 304; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 303;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 303; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 302;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 302; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 301;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 301; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 300;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 300; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 299;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 299; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 298;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 298; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 297;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 297; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 296;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 296; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 295;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 295; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 294;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 294; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 293;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 293; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 292;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 292; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 291;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 291; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 290;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 290; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-138-434A-3	
Query Match Similarity	
100.0%; Score 1657; DB 4; Length 289;	
Best Local Similarity	
100.0%; Pred. No. 8.9e-159;	
Matches 289; Conservative	
0; Mismatches 0; Indels 0; Gaps 0;	
Organism: Homo sapiens	
US-10-1	

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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:58:01 ; Search time 46 Seconds
(without alignments)
56.351 Million cell updates/sec

Title: US-10-666-851-2
Perfect score: 1706
Sequence: 1 MGIGRSEGRRGAGLGVIA.....KNFKMKMNHECPTFQSVFK 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Issued_Patents_AA:*
- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTRS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. 18 the number of result predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1701	99.7	314	2 US-08-937-057-7
2	1691.5	99.2	313	2 US-09-514-885-1
3	1691.5	99.2	313	2 US-09-942-016-6299
4	1657.5	97.2	313	2 US-09-546-043-3
5	1657.5	97.2	338	2 US-09-546-043-4
6	1629	95.5	314	2 US-09-087-0318-3
7	1614.5	94.5	313	2 US-09-087-0318-4
8	1267.5	74.3	267	2 US-09-546-043-7
9	1171	68.6	246	2 US-09-546-043-6
10	971	56.9	229	2 US-09-546-043-8
11	924.5	54.2	317	2 US-08-937-067-6
12	924.5	54.2	317	2 US-08-949-016-6300
13	911.5	53.4	305	2 US-09-943-016-7706
14	887.5	52.0	295	2 US-09-546-043-5
15	605.5	35.5	295	2 US-08-937-067-5
16	598	35.1	295	2 US-09-999-833A-415
17	598	35.1	295	2 US-10-020-445A-415
18	597	35.0	295	2 US-03-148-545-179
19	597	35.0	295	2 US-03-621-011-179
20	597	35.0	296	2 US-09-148-545-237
21	597	35.0	296	2 US-03-621-011-237
22	594	34.8	109	2 US-03-087-0318-19
23	508.5	29.8	295	2 US-08-893-654B-6
24	436.5	25.6	212	2 US-08-937-067-4
25	409.5	24.0	280	2 US-08-893-654B-4
26	387	22.7	281	2 US-08-893-654B-2
27	20.7	113	2 US-08-087-0318-24	

RESULT 1
US-08-937-067-7
Sequence 7, Application US/08937067
Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umansky, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING PEPTIDES ENCODED THEREBY AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Lehmarck, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-937-067-7

Query Match 99.7%; Score 1701; DB 2; Length 314;
Best Local Similarity 99.7%; Prod. No. 3.5e-174;
Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIGRSEGRRGAGLGVIA.....KNFKMKMNHECPTFQSVFK 60
Db 1 MGIGRSEGRRGAGLGVIA.....KNFKMKMNHECPTFQSVFK 60

Om Protein - protein search, using sw model						
Run on: May 5, 2006, 14:09:22 ; Search time 29 seconds (without alignment)						US-09-53-110-4672
Copyright (c) 1993 - 2006 Bioceleration Ltd.						29 41 52.6 245 2 US-09-134-001C-5651
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5						31 41 52.6 515 2 US-09-546-043-6
Searched: 572060 seqs, 82675679 residues						32 41 52.6 639 2 US-09-949-016-434
Title: Perfect score: US-10-666-851-2_COPY_217_231						33 41 51.3 106 2 US-09-462-917A-130
Sequence: 1 XKGENDKKIVPKKKK 15						34 40 51.3 120 2 US-09-415-785A-114
Minimum DB seq length: 0						35 40 51.3 120 2 US-09-415-868-114
Maximum DB seq length: 200000000						36 40 51.3 120 2 US-09-415-900-114
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 500 summaries						37 40 51.3 120 2 US-09-415-968-114
Database : Issued_Patents_AA:*						38 40 51.3 120 2 US-09-415-986-114
1: /cgn2_6/pctoda/1/iaaa/5_COMB.pep:*						39 40 51.3 120 2 US-09-415-988-114
2: /cgn2_6/pctoda/1/iaaa/6_COMB.pep:*						40 40 51.3 120 2 US-09-415-989-114
3: /cgn2_6/pctoda/1/iaaa/7_COMB.pep:*						41 40 51.3 120 2 US-09-415-990-114
4: /cgn2_6/pctoda/1/iaaa/8_COMB.pep:*						42 40 51.3 120 2 US-09-415-991-114
5: /cgn2_6/pctoda/1/iaaa/9_COMB.pep:*						43 40 51.3 120 2 US-09-415-992-114
6: /cgn2_6/pctoda/1/iaaa/backfiles1.pep:*						44 40 51.3 120 2 US-09-415-993-114
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						45 40 51.3 120 2 US-09-415-994-114
SUMMARIES						
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1	78	100.0	229	2 US-09-546-043-8		
2	78	100.0	267	2 US-09-546-043-7		
3	78	100.0	313	2 US-09-087-031B-4		
4	78	100.0	313	2 US-09-546-043-3		
5	78	100.0	313	2 US-09-514-085-1		
6	78	100.0	313	2 US-09-949-622-99		
7	78	100.0	314	2 US-09-937-067-7		
8	78	100.0	314	2 US-09-937-031B-3		
9	78	100.0	318	2 US-09-546-043-4		
10	53	67.9	108	2 US-09-10-433-788		
11	46	59.9	1014	2 US-09-319-588C-6		
12	45	57.7	305	2 US-09-949-016-7706		
13	45	57.7	317	2 US-09-937-067-6		
14	45	57.7	317	2 US-09-949-016-3300		
15	45	57.7	317	2 US-09-206-551-46		
16	44	56.4	324	2 US-09-248-796A-16963		
17	43	55.1	144	2 US-09-107-433-351		
18	43	55.1	316	2 US-09-270-767-34052		
19	43	55.1	316	2 US-09-270-767-42269		
20	42.5	54.5	106	2 US-09-513-999G-6072		
21	42	53.8	177	2 US-09-621-976-3338		
22	42	53.8	177	2 US-09-248-796A-14797		
23	42	53.8	1824	2 US-09-248-796A-14797		
24	42	53.8	1824	4 PCT-09-07261-16		
25	41	52.6	1663	4 PCT-US93-07261-16		
26	41	52.6	109	2 US-09-107-532A-1859		
27	41	52.6	117	2 US-09-438-185A-114		

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Run on: May 5, 2006, 14:10:16 ; Search time 12 Seconds (without alignments) 57.855 Million cell updates/sec																	
Title: US-10-666-851-2_COPY_217_231																	
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Scoring table: BL0SUM62 Gapop 10.0 , Gapext 0.5																	
Searched: 235405 seqs, 46284737 residues																	
Total number of hits satisfying chosen parameters: 231405																	
Minimum DB seq length: 0																	
Maximum DB seq length: 200000000																	
Post-processing: Maximum Match 0‡																	
Listing first 500 summaries																	
Database :																	
Published Applications AA_New:*																	
1:	/SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pepl:*																
2:	/SIDSS5/ptodata/1/pubpaa/US06_NEW_PUB.pepl:*																
3:	/SIDSS5/ptodata/1/pubpaa/US07_NEW_PUB.pepl:*																
4:	/SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pepl:*																
5:	/SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB.pepl:*																
6:	/SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB.pepl:*																
7:	/SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pepl:*																
8:	/SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pepl:*																
9:	/SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pepl:*																
10:	/SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pepl:*																
11:	/SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pepl:*																
12:	/SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB.pepl:*																
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.																	
SUMMARIES																	
Result No.	Score	Query Match Length	DB ID	Description													
1	78	100.0	413 9 US-10-821-234-989	Sequence 989, App	73	47.4	295	11 US-11-096-568A-341									
2	43.5	55.8	502 11 US-11-087-099-8879	Sequence 8879, App	74	47.4	335	11 US-11-096-568A-342									
3	42	53.8	189 11 US-11-188-298-518	Sequence 6518, App	75	47.4	361	11 US-11-096-568A-322									
4	42	53.8	500 9 US-10-517-151-4	Sequence 4, App	76	47.4	365	11 US-11-096-568A-323									
5	42	53.8	540 11 US-11-087-099-890	Sequence 690, App	77	47.4	377	11 US-11-096-568A-324									
6	42	53.8	540 11 US-11-087-099-1162	Sequence 4162, App	78	47.4	430	11 US-11-126-313-36									
7	42	53.8	541 11 US-11-087-099-1152	Sequence 2152, App	79	47.4	504	11 US-11-087-099-1055									
8	41	52.6	263 11 US-11-079-463-5502	Sequence 8502, App	80	47.4	554	11 US-11-098-686-1116									
9	41	52.6	278 11 US-11-079-463-6742	Sequence 6742, App	81	47.4	560	11 US-11-087-099-582									
10	41	52.6	375 11 US-11-096-568A-21506	Sequence 21506, App	82	47.4	560	11 US-11-108-298-1780									
11	41	52.6	409 9 US-10-533-811-57	Sequence 57, App	83	47.4	581	11 US-10-511-913-2597									
12	41	52.6	472 11 US-11-045-004-999	Sequence 999, App	84	47.4	602	11 US-11-169-041-205									
13	41	52.6	474 11 US-11-096-568A-21505	Sequence 21505, App	85	47.4	602	11 US-11-096-568A-304									
14	41	52.6	544 11 US-11-096-568A-21504	Sequence 21504, App	86	47.4	616	11 US-11-056-568A-303									
15	41	52.6	545 11 US-11-087-099-951	Sequence 951, App	87	47.4	616	11 US-11-096-568A-304									
16	41	52.6	547 11 US-11-087-099-034	Sequence 3034, App	88	47.4	651	11 US-11-108-298-1780									
17	41	52.6	723 11 US-11-045-004-1839	Sequence 1839, App	89	47.4	651	11 US-11-126-313-35									
18	40	51.3	35 11 US-11-096-725-1	Sequence 1, App	90	47.4	674	11 US-11-096-568A-305									
19	40	51.3	289 9 US-10-853-874-6740	Sequence 6740, App	91	47.4	674	11 US-11-096-568A-306									
20	40	51.3	611 9 US-10-793-626-2586	Sequence 8, App	92	46.8	674	11 US-11-072-512-3931									
21	40	51.3	611 9 US-10-793-626-2586	Sequence 2586, App	93	46.2	674	11 US-11-072-512-3931									

Sequence 12, App
Sequence 7, Appl
Sequence 9, Appl
Sequence 11, Appl
Sequence 632, App
Sequence 2534, App
Sequence 25726, A
Sequence 144, App
Sequence 145, App
Sequence 25724, A
Sequence 271, App
Sequence 6245, App
Sequence 1573, App
Sequence 318, App
Sequence 21, Appl
Sequence 323, App
Sequence 328, App
Sequence 117, App
Sequence 118, App
Sequence 8631, App
Sequence 161, App
Sequence 14800, A
Sequence 201, App
Sequence 14717, A
Sequence 25432, A
Sequence 19979, A
Sequence 6738, App
Sequence 29784, A
Sequence 2, Appl
Sequence 29783, A
Sequence 29782, A
Sequence 3443, App
Sequence 10056, A
Sequence 11963, A
Sequence 10067, A
Sequence 4419, App
Sequence 4418, App
Sequence 9706, App
Sequence 8519, App
Sequence 975, App
Sequence 1368, App
Sequence 7169, App
Sequence 11537, A
Sequence 34149, A
Sequence 34148, A
Sequence 34147, A
Sequence 32562, A
Sequence 32561, A
Sequence 32560, A
Sequence 17882, A
Sequence 35, Appl
Sequence 36, App
Sequence 1053, App
Sequence 1102, A
Sequence 5820, App
Sequence 2597, App
Sequence 205, App
Sequence 35, Appl
Sequence 36, App
Sequence 30450, A
Sequence 30450, A
Sequence 1, Appl
Sequence 23, Appl
Sequence 627, App
Sequence 630, App
Sequence 10024, A
Sequence 1758, App
Sequence 3937, App

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GanCore version 5.1.7

Run on: May 5, 2006, 14:06:21 ; Search time 38 Seconds
(without alignments)
37,980 Million cell updates/sec

OM protein - protein search, using sw model
Title: US-10-666-851-2_COPY_217_231
Perfect score: 78
Sequence: 1 KKEENGDKKVPKKCK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 Seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 20000000

Post-processing: Maximum Match 0%
Listing first 500 summaries

Database : PIR_80;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	46	59.0	205 T20990	hypothetical prote
2	46	59.0	279 T20987	hypothetical prote
3	46	59.0	397 T20013	hypothetical prote
4	46	59.0	3488 T34410	hypothetical prote
5	45	57.7	65 C69792	hypothetical prote
6	45	57.7	317 J80175	frazzled protein-1
7	44	56.4	502 T22045	hypothetical prote
8	43.5	55.8	502 T14286	embryogenic callus
9	43	55.1	132 T48278	hypothetical prote
10	43	55.1	175 T05669	hypothetical prote
11	43	55.1	245 T50399	hypothetical prote
12	43	55.1	690 E72337	translation initia
13	43	55.1	196 T22832	protein-tirosine k
14	43	55.1	1278 A71609	probable secreted
15	42	53.8	95 G97706	hypothetical prote
16	42	53.8	183 A35270	ribosomal protein
17	42	53.8	288 S26495	transcription fact
18	42	53.8	295 T86371	hypothetical prote
19	42	53.8	367 T139172	cyclin-dependent k
20	42	53.8	625 A90127	hypothetical prote
21	42	53.8	734 T23647	hypothetical prote
22	42	53.8	751 S65469	DNA topoisomerase
23	42	53.8	806 T23648	hypothetical prote
24	42	53.8	881 T49279	hypothetical prote
25	42	53.8	1063 T38732	probable helicase
26	42	53.8	2441 D71623	erythrocyte membra
27	41.5	53.2	239 A9291	hypothetical prote
28	41.5	53.2	422 H90271	hypothetical prote
29	41.5	53.2		

30	41.5	53.2	422 H90275	hypothetical prote
31	41	52.6	109 A86505	L31 ribosomal prot
32	41	52.6	109 H72118	ribosomal protein
33	41	52.6	2 S01281	hypothetical prote
34	41	52.6	200 B5057	RNA polymerase (de
35	41	52.6	200 E97926	hypothetical prote
36	41	52.6	224 T39771	6-Phosphogluconate
37	41	52.6	277 D97067	hypothetical prote
38	41	52.6	285 T22458	probable xylose-
39	41	52.6	399 T22933	hypothetical prote
40	41	52.6	400 AB1565	cell division prote
41	41	52.6	400 AC1241	6-Phosphogluconate
42	41	52.6	472 AH1246	hypothetical prote
43	41	52.6	549 T23526	DNA topoisomerase
44	41	52.6	552 S48328	hypothetical prote
45	41	52.6	648 T27412	hypothetical prote
46	41	52.6	723 AG1603	polynucleotide pho
47	41	52.6	723 F6061	ribonucleotide red
48	41	52.6	743 H97302	hypothetical prote
49	41	52.6	769 ISBYT1	hypothetical prote
50	41	51.9	1359 T34036	hypothetical prote
51	40	51.9	148 T6761	F2214.5 protein -
52	40	51.9	155 T16753	hypothetical prote
53	40	51.9	203 T01688	HIV-1 retroprote
54	40	51.9	235 AD1735	HIV-1 retroprote
55	40	51.9	251 T39332	HIV-1 retroprote
56	40	51.9	278 S67432	HIV-1 retroprote
57	40	51.9	289 T84098	HIV-1 retroprote
58	40	51.9	61 T41257	HIV-1 retroprote
59	40	51.9	62 D71615	HIV-1 retroprote
60	40	51.9	76 T16592	HIV-1 retroprote
61	40	51.9	80 C96608	HIV-1 retroprote
62	40	51.9	820 C81252	HIV-1 retroprote
63	40	51.9	839 T16753	HIV-1 retroprote
64	40	51.9	902 T01688	HIV-1 retroprote
65	40	51.9	912 S33980	HIV-1 retroprote
66	40	51.9	1002 GN14ND	HIV-1 retroprote
67	40	51.9	1002 S54378	HIV-1 retroprote
68	40	51.9	1003 GNVWLY	HIV-1 retroprote
69	40	51.9	1003 B44021	HIV-1 retroprote
70	40	51.9	1003 T09440	HIV-1 retroprote
71	40	51.9	1003 T09440	HIV-1 retroprote
72	40	51.9	1003 T09440	HIV-1 retroprote
73	40	51.9	1003 T09440	HIV-1 retroprote
74	40	51.9	1003 T09440	HIV-1 retroprote
75	40	51.9	1003 T09440	HIV-1 retroprote
76	40	51.9	1012 GNVWHL	HIV-1 retroprote
77	40	51.9	1015 S02160	HIV-1 retroprote
78	40	51.9	1447 S02160	DNA topoisomerase
79	40	51.9	1545 T71841	multidrug resistant
80	40	51.9	1851 T13904	calcium channel al
81	40	51.9	2515 A41519	posterior-group pr
82	40	51.9	2938 T30249	cell proliferation
83	40	50.0	78 WZVZG3	G3L protein - Amra
84	39	50.0	101 G90536	Hypothetical prote
85	39	50.0	152 S22323	histone H2B - whea
86	39	50.0	169 AD3110	transcription regu
87	39	50.0	179 S61904	hypothetical prote
88	39	50.0	201 H98176	transcription regu
89	39	50.0	39 T00865	hypothetical prote
90	39	50.0	101 G90536	hypothetical prote
91	39	50.0	226 S41032	ribosomal protein
92	39	50.0	277 AE1403	ribosomal protein
93	39	50.0	277 AD1779	ribosomal protein
94	39	50.0	298 G96773	hypothetical prote
95	39	50.0	321 T39278	hypothetical prote
96	39	50.0	392 T19327	hypothetical prote
97	39	50.0	411 B89665	ribosomal protein
98	39	50.0	477 T21421	hypothetical prote
99	39	50.0	500 A46101	protein-tirosine-p
100	39	50.0	542 S62508	protein-tirosine-p
101	39	50.0	548 B46101	protein-tirosine-p
102	39	50.0	557 T04465	hypothetical prote

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: May 5, 2006, 14:02:56 ; Search time 226 Seconds

(without alignments)
 46.827 Million cell updates/sec

Title: US-10-666-851-2_COPY_217_231
 Perfect score: 78
 Sequence: 1 KKENGDKLKVPKKK 15

Scoring table: BLASTM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70552306 residues

Total number of hits satisfying chosen parameters:

2166443

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : UniProt_05_80_*
 1: uniprot_sprot_*
 2: uniprot_trembl_*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	78	100.0	158	1 SFRP1_RAT	Q9R168 rattus norv
2	78	100.0	178	2 O6ZS14_HUMAN	O6z14 homo sapien
3	78	100.0	308	1 SFRP1_BOVIN	O91166 bov tauris
4	78	100.0	314	1 SFRP1_HUMAN	O8n74 homo sapien
5	78	100.0	314	1 SFRP1_MOUSE	O8cau3 mus musculus
6	78	100.0	314	1 SFRP1_MOUSE	O55ka2 mus musculus
7	64	82.1	314	1 SFRP1_CHICK	O9d6q4 gallus gallus
8	58	74.4	5229	2 QTRT4_PLAVO	O7rfq4 plasmid
9	51	65.4	536	2 O6CC4_9ARCH	064cc4 uncultured
10	50	64.1	311	2 Q9Y124_XENIA	Q9y124 xenopus lae
11	49	62.8	287	2 O614B0_CASER	O614a0 caenorhabdit
12	49	62.8	308	2 O5YF5_ENTH1	O5Yf5 entamoeba h
13	49	62.8	326	2 O5Q0F4_ENTH1	O5q0f4 entamoeba h
14	49	62.8	758	2 O4RUV9_TEETNG	O4ruv9 tetradon
15	48	61.5	310	2 O6NBR8_BRABR	O6nbr8 brachydanio
16	48	61.5	321	2 O4SKK3_TETNG	O4skk3 tetraodon
17	47	60.3	297	2 O82W10_NITRUE	O82w10 nitrosomona
18	47	60.3	348	2 O7P45_PLAVO	O7p45 plasmid
19	47	60.3	425	2 O4YPAB_PLAVO	O4ypab plasmid
20	47	60.3	425	2 O6LTH8_ARATH	O6lth8 arabidopsis
21	46	59.0	136	2 O9W6A_9HTWL	O9w6a human immun
22	46	59.0	261	2 Q4Y8S7_PLAVO	Q4y8s7 plasmid
23	46	59.0	278	2 O814L0_CASBL	O814l0 caenorhabdi
24	46	59.0	279	2 YST1_CHEEL	O10033 caenorhabdi
25	46	59.0	286	2 O909N2_9HTWL	O909n2 human immun
26	46	59.0	315	2 O8AWG4_XENIA	O8awg4 xenopus lae
27	46	59.0	315	2 O66703_XENIA	O66703 xenopus lae
28	46	59.0	315	2 O6GL50_XENIA	O6gl50 xenopus tro
29	46	59.0	324	2 O54Q96_DICOR	O54q96 dictyoscelli
30	46	59.0	377	2 O425H0_PLAVO	O425h0 plasmid
31	46	59.0	397	1 YXX7_CAEABL	O18674 caenorhabdi

OM protein - protein search, using sw model	GenCore version 5.1.7	Copyright (c) 1993 - 2006 Biocceleration Ltd.
Run on:	May 5, 2006, 14:10:03 ; Search time 76 Seconds (without alignments)	82.466 Million cell updates/sec
Title:	US-10-666-851-2_COPY_217_231	
Perfect score:	78	4 US-10-425-115-2343409
Sequence:	1 KKEENGDKIVPKKK 15	Sequence 243409, Sequence 126220, Sequence 204843, Sequence 238136, Sequence 365021, Sequence 275080, Sequence 208855, Sequence 301158, Sequence 276281, Sequence 6, Appli
Scoring table:	BLOSUM62	Sequence 20729, Sequence 188977, Sequence 51035, A Sequence 223433, Sequence 351455, Sequence 197216, Sequence 273759, Sequence 20729, Sequence 280739, Sequence 262112, Sequence 6, Appli Sequence 2, Appli Sequence 1, Appli Sequence 148923, Sequence 341736, Sequence 124929, Sequence 236534, Sequence 164574, Sequence 208959, Sequence 231259, Sequence 278506, Sequence 193907, Sequence 224408, Sequence 362096, Sequence 182779, Sequence 52041, A Sequence 150171, Sequence 22725, Sequence 338001, Sequence 275569, Sequence 136903, Sequence 4505, AP Sequence 7334, AP Sequence 34771, Sequence 234601, Sequence 289895, Sequence 252065, Sequence 196660, Sequence 125118, Sequence 286620, Sequence 192731, Sequence 261445, Sequence 321817, Sequence 231813, Sequence 112709, Sequence 353271, Sequence 165932, Sequence 225875, Sequence 224765, Sequence 235573, Sequence 239967, Sequence 316426, Sequence 281841, Sequence 285850, Sequence 174485, Sequence 266013, Sequence 3451, AP Sequence 336591, Sequence 112626, Sequence 164595,
Searched:	1867569 seqs, 417829326 residues	
Total number of hits satisfying chosen parameters:	1867569	
Minimum DB seq length: 0		
Maximum DB seq length: 200000000		
Post-processing: Minimum Match 0%		
Maximum Match 100%		
Listing first 500 summaries		
Database :	Published Applications AA_Main:*	
1:	/cgns_6/prodata/1/pupaa/us07_PUBCOMB.pep:*	
2:	/cgns_6/prodata/1/pupaa/us08_PUBCOMB.pep:*	
3:	/cgns_6/prodata/1/pupaa/us09_PUBCOMB.pep:*	
4:	/cgns_6/prodata/1/pupaa/us10_PUBCOMB.pep:*	
5:	/cgns_6/prodata/1/pupaa/us10_PUBCOMB.pep:*	
6:	/cgns_6/podata/1/pupaa/us11_PUBCOMB.pep:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	1	
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OM protein - protein search, using sw model

Run on: May 5, 2006, 14:02:26 ; Search time 184 seconds
(without alignments)
(35,819 Million cell updates/sec)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: US-10-666-851-2_COPY_217_231
perfect score: 78
Sequence: 1 KKENGDKKAVPKKKK 15

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 500 summaries

Database : A_Genesed 21:*

1: genesedp1980s:*

2: genesedp1990s:*

3: genesedp2000s:*

4: genesedp2001s:*

5: genesedp2002s:*

6: genesedp2003ab:*

7: genesedp2003ba:*

8: genesedp2004s:*

9: genesedp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	% Match	Length	DB ID	Description
1	78	100.0	141	5	ABR82254	Abbr82254 Human SFR
2	78	100.0	148	2	ARY48493	Ray8493 Human bre
3	78	100.0	178	8	ADR09139	Adr09139 Human pro
4	78	100.0	229	5	ABR82249	Abbr82249 Human sec
5	78	100.0	229	7	ADCT7191	Adct7191 Deletion
6	78	100.0	229	8	ADH43313	Adh43313 Human sec
7	78	100.0	267	5	ABB2248	Abb2248 Human sec
8	78	100.0	267	7	ADCT7190	Adct7190 Deletion
9	78	100.0	267	8	ADH43312	Adh43312 Human sec
10	78	100.0	313	4	AHE0154	Ahe0154 Human sec
11	78	100.0	313	4	ARU07695	Aru07695 Human Pri
12	78	100.0	313	5	ABBB2244	Abbb2244 Human sec
13	78	100.0	313	8	ABP72784	Abp72784 Human sec
14	78	100.0	313	7	ABR64248	Abbr64248 Human sec
15	78	100.0	313	7	ADCT71186	Adct71186 Human sec
16	78	100.0	313	8	ADH43308	Adh43308 Human sec
17	78	100.0	313	8	ADP68541	Adp68541 Human sec
18	78	100.0	313	8	ADU08603	Adu08603 Human sec
19	78	100.0	313	8	ABE4566	Abe4566 Human lyp
20	78	100.0	313	9	ADV44910	Adv44910 Secreted
21	78	100.0	313	9	ADX58916	Adx58916 Human reg
22	78	100.0	314	2	AWW82817	Awaw82817 Human sec
23	78	100.0	314	2	ABW88228	Abw88228 Human Pri
24	78	100.0	314	6	ABP72785	Abp72785 Human sec

25	78	100.0	314	6	ABP72783	Abp72783 Human SFR
26	78	100.0	314	7	ABP61429	Abp61429 Murine em
27	78	100.0	314	7	ABR1427	Abx61427 Murine em
28	78	100.0	314	8	ADP8536	Adp68536 Human sec
29	78	100.0	314	8	ADP9142	Adp99142 Secreted
30	78	100.0	314	8	ADU86506	Adu86506 Mouse sec
31	78	100.0	338	5	ABR82245	Abbr82245 Human sec
32	78	100.0	338	7	ADC71187	Adc71187 Human SFR
33	78	100.0	338	8	ADH43309	Adh43309 Human SFR
34	78	100.0	362	8	ABM82799	Abm82799 Human dia
35	53	67.9	108	9	ADB96153	Adb96153 Novel S.
36	53	67.9	108	9	ABA60023	Aeb60023 Streptoco
37	49	62.8	110	4	AAU05308	Aau05308 Human pol
38	48	61.5	121	4	AAU05517	Aau05517 Human pol
39	47	60.3	31	2	AAW12916	Aaw12916 Octopepti
40	46	59.0	128	4	AAU04686	Aau04686 Human pol
41	46	59.0	194	6	ADK39977	Adk39977 HIV Pol
42	46	59.0	1002	9	ADK39946	Adk39946 HIV Pol
43	46	59.0	1003	9	ADK39998	Adk39998 HIV Pol
44	46	59.0	1011	9	ADK0087	Adk40087 HIV Pol
45	46	59.0	1014	2	ARW68474	HIV-1 str
46	46	59.0	1014	2	ADP86062	Adp56062 Human PRO
47	45	57.7	194	6	ABU23111	Abu23111 Protein e
48	45	57.7	317	2	ARW73507	Awaw73507 Human ATG
49	45	57.7	317	2	AAW37816	Aaw37816 Human sec
50	45	57.7	317	8	ADM67242	Adm67242 Human hom
51	45	57.7	317	8	ADP86062	Adp56062 Human PRO
52	45	57.7	317	8	ADP86062	Adp56062 Human PRO
53	45	57.7	1018	3	ABA01769	Aab01769 Simian im
54	44	56.4	122	4	AAU03187	Aac02187 Human pol
55	44	56.4	587	5	ABP73497	Abp73497 Candida a
56	43	55.1	111	4	AAU02430	Aao02430 Human pol
57	43	55.1	121	3	ARG14889	Aeg1489 Arabidops
58	43	55.1	137	4	AAU03896	Aao03896 Human pol
59	43	55.1	143	3	AGA14888	Aag14888 Arabidops
60	43	55.1	144	8	ADP84816	Adp54816 Novel S.
61	43	55.1	144	9	ABA88686	Aea88686 Streptoco
62	43	55.1	1002	9	ADK40058	Adk40058 HIV Pol
63	43	55.1	1278	3	ABR18277	Aab18277 Plasmodiu
64	42.5	54.5	65	3	AAU01991	Aag01991 Human sec
65	42	53.8	66	4	AAU03273	Aao03273 Human pol
66	42	53.8	137	4	AAU02310	Aao02310 Human pol
67	42	53.8	190	3	ARG25277	Aag25277 Arabidops
68	42	53.8	195	3	AAU03061	Aao33061 Arabidops
69	42	53.8	225	7	ADR31137	Ado31137 Human dia
70	42	53.8	250	5	ABG99159	Aabg99159 Human end
71	42	53.8	272	3	AGA49440	Aag49440 Arabidops
72	42	53.8	274	3	AAU05974	Aab06974 Arabidops
73	42	53.8	292	4	ABP51977	Abp51977 Drosophil
74	42	53.8	295	3	AAU04943	Aaa49439 Arabidops
75	42	53.8	297	3	AAU05973	Aag06973 Arabidops
76	42	53.8	314	8	ADA67241	Adm67241 Murine ad
77	42	53.8	314	8	ADU05987	Adas3987 Human Cdk
78	42	53.8	367	6	ADU05987	Adas3987 Human Cdk
79	42	53.8	369	4	AAU07489	Aam79489 Human pro
80	42	53.8	369	4	AAU07489	Aam79489 Human pol
81	42	53.8	369	4	AAU07489	Aam79489 Human pol
82	42	53.8	424	4	ABD64443	Abb64443 Drosophil
83	42	53.8	455	7	ADC1549	Adc1549 Human nov
84	42	53.8	476	4	AAU07505	Aam78505 Human pro
85	42	53.8	500	4	AAU07505	Aam78505 Human pro
86	42	53.8	500	5	ABP95660	Abp95660 Human nuc
87	42	53.8	500	8	ADH44815	Adh44816 Human KRZ
88	42	53.8	500	8	ADL32095	Adl12095 Human pro
89	42	53.8	734	8	ADN22640	Adn22640 Bacterial
90	42	53.8	805	8	ADN22639	Adn22639 Bacterial
91	42	53.8	846	4	AMJ39803	Aam39803 Human pol
92	42	53.8	861	5	ABP95660	Abp95660 Human nuc
93	42	53.8	881	5	ABP95593	Abp95593 Rice bicida
94	42	53.8	887	7	ABM88655	Abm88655 Rice abio
95	42	53.8	920	7	ABM90383	Abm90383 Rice abio
96	42	53.8	955	4	AMM39802	Aam39802 Human pol
97	42	53.8	1146	8	ADP99073	Adp99073 C. albica

